

SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
Yu, Xuanchuan
Friddle, Carl Johan
Miranda, Miracar
Gerhardt, Brenda
Mathur, Brian

<120> Novel Human Ig-Domain Proteins and Polynucleotides Encoding the Same

<130> LEX-0299-USA

<150> US 60/267,583

<151> 2001-02-09

<160> 11

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 936

<212> DNA

<213> homo sapiens

<400> 1

```
atggcctttc ttgtggetca ccctatgcag tttgtgtatt tgttgacaac tttatgtgtt 60
tttaatatgg tttttgccaa acttggtttt tccgagaccg tcttttctca gaggctcagt 120
tttaccgtcc tatctgcagt cggctacttt cagtggcaga agaggccaca tctgcttcct 180
gtaggccctc tgggcagaag catgcgctgg tgtctcctcc tgatctgggc ccaggggctg 240
aggcaggctc ccctcgctc aggaatgatg acaggcacia tagaaacaac ggggaacatt 300
tctgcagaga aaggtggctc tatcatctta caatgtcacc tctcctccac cacggcacia 360
gtgacccagg tcaactggga gcagcaggac cagcttctgg ccatttgtaa tgctgacttg 420
gggtggcaca tctccccatc cttcaaggat cgagtggccc caggtcccgg cctgggcctc 480
accctccagt cgctgaccgt gaacgataca ggggagtact tctgcatcta tcacacctac 540
cctgatggga cgtacactgg gagaatcttc ctggaggctc tagaaagctc agtggctgag 600
cacggtgccg ggttccagat tccattgctt ggagccatgg ccgcgacgct ggtggctcct 660
tgcacagcag tcatcgttgt ggtcgcgttg actagaaaga agaaagccct cagaatccat 720
tctgtggaag gtgacctcag gagaaaatca gctggacagg aggaatggag cccagtgct 780
ccctcacccc caggaagctg tgtccaggca gaagctgcac ctgctgggct ctgtggagag 840
cagcggggag aggactgtgc cgagctgcat gactacttca atgtcctgag ttacagaagc 900
ctgggtaact gcagcttctt cacagagact ggtag 936
```

<210> 2

<211> 311

<212> PRT

<213> homo sapiens

<400> 2

```
Met Ala Phe Leu Val Ala His Pro Met Gln Phe Val Tyr Leu Leu Thr
  1             5             10             15
Thr Leu Cys Val Phe Asn Met Val Phe Ala Lys Leu Gly Phe Ser Glu
      20             25             30
Thr Val Phe Ser Gln Arg Leu Ser Phe Thr Val Leu Ser Ala Val Gly
      35             40             45
```

Tyr Phe Gln Trp Gln Lys Arg Pro His Leu Leu Pro Val Gly Pro Leu
50 55 60
Gly Arg Ser Met Arg Trp Cys Leu Leu Leu Ile Trp Ala Gln Gly Leu
65 70 75 80
Arg Gln Ala Pro Leu Ala Ser Gly Met Met Thr Gly Thr Ile Glu Thr
85 90 95
Thr Gly Asn Ile Ser Ala Glu Lys Gly Gly Ser Ile Ile Leu Gln Cys
100 105 110
His Leu Ser Ser Thr Thr Ala Gln Val Thr Gln Val Asn Trp Glu Gln
115 120 125
Gln Asp Gln Leu Leu Ala Ile Cys Asn Ala Asp Leu Gly Trp His Ile
130 135 140
Ser Pro Ser Phe Lys Asp Arg Val Ala Pro Gly Pro Gly Leu Gly Leu
145 150 155 160
Thr Leu Gln Ser Leu Thr Val Asn Asp Thr Gly Glu Tyr Phe Cys Ile
165 170 175
Tyr His Thr Tyr Pro Asp Gly Thr Tyr Thr Gly Arg Ile Phe Leu Glu
180 185 190
Val Leu Glu Ser Ser Val Ala Glu His Gly Ala Arg Phe Gln Ile Pro
195 200 205
Leu Leu Gly Ala Met Ala Ala Thr Leu Val Val Ile Cys Thr Ala Val
210 215 220
Ile Val Val Val Ala Leu Thr Arg Lys Lys Lys Ala Leu Arg Ile His
225 230 235 240
Ser Val Glu Gly Asp Leu Arg Arg Lys Ser Ala Gly Gln Glu Glu Trp
245 250 255
Ser Pro Ser Ala Pro Ser Pro Pro Gly Ser Cys Val Gln Ala Glu Ala
260 265 270
Ala Pro Ala Gly Leu Cys Gly Glu Gln Arg Gly Glu Asp Cys Ala Glu
275 280 285
Leu His Asp Tyr Phe Asn Val Leu Ser Tyr Arg Ser Leu Gly Asn Cys
290 295 300
Ser Phe Phe Thr Glu Thr Gly
305 310

<210> 3
<211> 672
<212> DNA
<213> homo sapiens

<400> 3
atgatgacag gcacaataga aacaacgggg aacatttctg cagagaaagg tggctctatc 60
atcttacaat gtcacctctc ctccaccacg gcacaagtga cccagggtcaa ctgggagcag 120
caggaccagc ttctggccat ttgtaatgct gacttggggg ggcacatctc cccatccttc 180
aaggatcgag tggccccagg tcccggcctg ggcctcacc tccagtcgct gaccgtgaac 240
gatacagggg agtacttctg catctatcac acctaccctg atgggacgta cactgggaga 300
atcttcctgg aggtcctaga aagctcagtg gctgagcacg gtgccagggt ccagattcca 360
ttgcttggag ccatggccgc gacgctgggt gtcacttgca cagcagtcac cgtggtgggtc 420
gcgttgacta gaaagaagaa agccctcaga atccattctg tggaagggtga cctcaggaga 480
aatcagctg gacaggagga atggagcccc agtgctccct caccgccagg aagctgtgtc 540
caggcagaag ctgcacctgc tgggctctgt ggagagcagc ggggagagga ctgtgccgag 600
ctgcatgact acttcaatgt cctgagttac agaagcctgg gtaactgcag cttcttcaca 660
gagactgggt ag 672

<210> 4

<211> 223
 <212> PRT
 <213> homo sapiens

<400> 4
 Met Met Thr Gly Thr Ile Glu Thr Thr Gly Asn Ile Ser Ala Glu Lys
 1 5 10 15
 Gly Gly Ser Ile Ile Leu Gln Cys His Leu Ser Ser Thr Thr Ala Gln
 20 25 30
 Val Thr Gln Val Asn Trp Glu Gln Gln Asp Gln Leu Leu Ala Ile Cys
 35 40 45
 Asn Ala Asp Leu Gly Trp His Ile Ser Pro Ser Phe Lys Asp Arg Val
 50 55 60
 Ala Pro Gly Pro Gly Leu Gly Leu Thr Leu Gln Ser Leu Thr Val Asn
 65 70 75 80
 Asp Thr Gly Glu Tyr Phe Cys Ile Tyr His Thr Tyr Pro Asp Gly Thr
 85 90 95
 Tyr Thr Gly Arg Ile Phe Leu Glu Val Leu Glu Ser Ser Val Ala Glu
 100 105 110
 His Gly Ala Arg Phe Gln Ile Pro Leu Leu Gly Ala Met Ala Ala Thr
 115 120 125
 Leu Val Val Ile Cys Thr Ala Val Ile Val Val Val Ala Leu Thr Arg
 130 135 140
 Lys Lys Lys Ala Leu Arg Ile His Ser Val Glu Gly Asp Leu Arg Arg
 145 150 155 160
 Lys Ser Ala Gly Gln Glu Glu Trp Ser Pro Ser Ala Pro Ser Pro Pro
 165 170 175
 Gly Ser Cys Val Gln Ala Glu Ala Ala Pro Ala Gly Leu Cys Gly Glu
 180 185 190
 Gln Arg Gly Glu Asp Cys Ala Glu Leu His Asp Tyr Phe Asn Val Leu
 195 200 205
 Ser Tyr Arg Ser Leu Gly Asn Cys Ser Phe Phe Thr Glu Thr Gly
 210 215 220

<210> 5
 <211> 1821
 <212> DNA
 <213> homo sapiens

<400> 5
 atgcttcaca cggccatata atgctggcag ccattcctgg gtctggctgt ggtgttaata 60
 ttcattgggat ccaccattgg ctgccccgct cgctgtgagt gctctgcca gaacaaatct 120
 gtttagctgtc acagaaggcg attgatcgcc atcccagagg gcattcccat cgaaaccaa 180
 atcttggacc tcagtaaaaa caggctaaaa agcgtcaacc ctgaagaatt catatcatat 240
 cctctgctgg aagagataga cttgagtgc aacatcattg ccaatgtgga accaggagca 300
 ttcaacaatc tctttaacct gcgttcctc cgctaaaag gcaatcgtct aaagctggtc 360
 cctttgggag tattcacggg gctgtccaat ctactaagc ttgacattag tgagaataag 420
 attgtcattt tactagacta catgttccaa gatctacata acctgaagtc tctagaagtg 480
 ggggacaatg atttggttta tatatcacac agggcattca gtgggcttct tagcttgagg 540
 cagctcaccc tggagaaatg caacttaaca gcagtaccaa cagaagccct ctcccacctc 600
 cgagcctca tcagcctgca tctgaagcat ctcaatatca acaatatgcc tgtgtatgcc 660
 tttaaaagat tgttccacct gaaacaccta gagattgact attggccttt actggatatg 720
 atgcctgcca atagcctcta cgggtctcaac ctacatccc tttcagtcac caacaccaat 780
 ctgtctactg tacccttctc tgcctttaa cacctggtat acctgactca ccttaacctc 840
 tctacaatc ccatcagcac tattgaagca ggcattgtct ctgacctgat ccgccttcag 900

gagcttcata tagtgggggc ccagcttcgc accattgagc ctcactcctt ccaaggggctc 960
 cgcttcctac gcgtgctcaa tgtgtctcag aacctgctgg aaactttgga agagaatgtc 1020
 ttctcctccc ctagggctct ggaggtcttg agcattaaca acaaccctct gccctgtgac 1080
 tgccgccttc tctggatctt gcagcgacag cccaccctgc agtttggtgg ccagcaacct 1140
 atgtgtgctg gcccagacac catccgtgag aggtctttca aggatttcca tagcactgcc 1200
 ctttcttttt actttacctg caaaaaaccc aaaatccgtg aaaagaagtt gcagcatctg 1260
 ctagtagatg aagggcagac agtccagcta gaatgcagtg cagatggaga cccgcagcct 1320
 gtgatttctt gggtgacacc ccgaaggcgt ttcacacca ccaagtccaa tggaagagcc 1380
 accgtgttgg gtgatggcac cttggaaatc cgctttgccc aggatcaaga cagcgggatg 1440
 tatgtttgca tcgctagcaa tgctgctggg aatgatacct tcacagcctc cttaactgtg 1500
 aaaggattcg cttcagatcg ttttctttat gcgaacagga cccctatgta catgaccgac 1560
 tccaatgaca ccatttccaa tggcaccaat gccaatactt tttccctgga ccttaaaaca 1620
 atactgggtg ctacagctat gggctgcttc acattcctgg gagtgggtttt attttgtttt 1680
 cttctccttt ttgtgtggag ccgagggaaa ggcaagcaca aaaacagcat tgaccttgag 1740
 tatgtgcca gaaaaaaca tggtgctggt gtggaagggg aggtagctgg acccaggagg 1800
 ttcaacatga aaatgatttg a 1821

<210> 6
 <211> 606
 <212> PRT
 <213> homo sapiens

<400> 6
 Met Leu His Thr Ala Ile Ser Cys Trp Gln Pro Phe Leu Gly Leu Ala
 1 5 10 15
 Val Val Leu Ile Phe Met Gly Ser Thr Ile Gly Cys Pro Ala Arg Cys
 20 25 30
 Glu Cys Ser Ala Gln Asn Lys Ser Val Ser Cys His Arg Arg Arg Leu
 35 40 45
 Ile Ala Ile Pro Glu Gly Ile Pro Ile Glu Thr Lys Ile Leu Asp Leu
 50 55 60
 Ser Lys Asn Arg Leu Lys Ser Val Asn Pro Glu Glu Phe Ile Ser Tyr
 65 70 75 80
 Pro Leu Leu Glu Glu Ile Asp Leu Ser Asp Asn Ile Ile Ala Asn Val
 85 90 95
 Glu Pro Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Ser Leu Arg Leu
 100 105 110
 Lys Gly Asn Arg Leu Lys Leu Val Pro Leu Gly Val Phe Thr Gly Leu
 115 120 125
 Ser Asn Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys Ile Val Ile Leu
 130 135 140
 Leu Asp Tyr Met Phe Gln Asp Leu His Asn Leu Lys Ser Leu Glu Val
 145 150 155 160
 Gly Asp Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu
 165 170 175
 Leu Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ala Val
 180 185 190
 Pro Thr Glu Ala Leu Ser His Leu Arg Ser Leu Ile Ser Leu His Leu
 195 200 205
 Lys His Leu Asn Ile Asn Asn Met Pro Val Tyr Ala Phe Lys Arg Leu
 210 215 220
 Phe His Leu Lys His Leu Glu Ile Asp Tyr Trp Pro Leu Leu Asp Met
 225 230 235 240
 Met Pro Ala Asn Ser Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Val
 245 250 255
 Thr Asn Thr Asn Leu Ser Thr Val Pro Phe Leu Ala Phe Lys His Leu

Val	Tyr	Leu	Thr	His	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	Thr	Ile
		275					280					285			
Glu	Ala	Gly	Met	Phe	Ser	Asp	Leu	Ile	Arg	Leu	Gln	Glu	Leu	His	Ile
	290					295					300				
Val	Gly	Ala	Gln	Leu	Arg	Thr	Ile	Glu	Pro	His	Ser	Phe	Gln	Gly	Leu
305					310					315					320
Arg	Phe	Leu	Arg	Val	Leu	Asn	Val	Ser	Gln	Asn	Leu	Leu	Glu	Thr	Leu
			325					330					335		
Glu	Glu	Asn	Val	Phe	Ser	Ser	Pro	Arg	Ala	Leu	Glu	Val	Leu	Ser	Ile
		340					345					350			
Asn	Asn	Asn	Pro	Leu	Ala	Cys	Asp	Cys	Arg	Leu	Leu	Trp	Ile	Leu	Gln
	355					360					365				
Arg	Gln	Pro	Thr	Leu	Gln	Phe	Gly	Gly	Gln	Gln	Pro	Met	Cys	Ala	Gly
	370				375					380					
Pro	Asp	Thr	Ile	Arg	Glu	Arg	Ser	Phe	Lys	Asp	Phe	His	Ser	Thr	Ala
385				390					395						400
Leu	Ser	Phe	Tyr	Phe	Thr	Cys	Lys	Lys	Pro	Lys	Ile	Arg	Glu	Lys	Lys
		405						410					415		
Leu	Gln	His	Leu	Leu	Val	Asp	Glu	Gly	Gln	Thr	Val	Gln	Leu	Glu	Cys
	420					425						430			
Ser	Ala	Asp	Gly	Asp	Pro	Gln	Pro	Val	Ile	Ser	Trp	Val	Thr	Pro	Arg
	435					440					445				
Arg	Arg	Phe	Ile	Thr	Thr	Lys	Ser	Asn	Gly	Arg	Ala	Thr	Val	Leu	Gly
	450					455				460					
Asp	Gly	Thr	Leu	Glu	Ile	Arg	Phe	Ala	Gln	Asp	Gln	Asp	Ser	Gly	Met
465				470					475						480
Tyr	Val	Cys	Ile	Ala	Ser	Asn	Ala	Ala	Gly	Asn	Asp	Thr	Phe	Thr	Ala
		485						490					495		
Ser	Leu	Thr	Val	Lys	Gly	Phe	Ala	Ser	Asp	Arg	Phe	Leu	Tyr	Ala	Asn
	500						505					510			
Arg	Thr	Pro	Met	Tyr	Met	Thr	Asp	Ser	Asn	Asp	Thr	Ile	Ser	Asn	Gly
	515					520						525			
Thr	Asn	Ala	Asn	Thr	Phe	Ser	Leu	Asp	Leu	Lys	Thr	Ile	Leu	Val	Ser
	530				535						540				
Thr	Ala	Met	Gly	Cys	Phe	Thr	Phe	Leu	Gly	Val	Val	Leu	Phe	Cys	Phe
545				550					555						560
Leu	Leu	Leu	Phe	Val	Trp	Ser	Arg	Gly	Lys	Gly	Lys	His	Lys	Asn	Ser
		565						570					575		
Ile	Asp	Leu	Glu	Tyr	Val	Pro	Arg	Lys	Asn	Asn	Gly	Ala	Val	Val	Glu
	580					585						590			
Gly	Glu	Val	Ala	Gly	Pro	Arg	Arg	Phe	Asn	Met	Lys	Met	Ile		
	595					600						605			

<210> 7
 <211> 1494
 <212> DNA
 <213> homo sapiens

<400> 7
 atgcttcaca cggccatatt atgctggcag ccattcctgg gtctggctgt ggtgttaatc 60
 ttcattgggat ccaccattgg ctgcccgcgt cgctgtgagt gctctgccca gaacaaatct 120
 gtttagctgtc acagaaggcg attgatcgcc atcccagagg gcattcccat cgaaacccaa 180
 atcttggacc tcagtaaaaa caggctaaaa agcgtcaacc ctgaagaatt catatcatat 240
 cctctgctgg aagagataga cttgagtgac aacatcattg ccaatgtgga accaggagca 300

```

ttcaacaatc tctttaacct gcgttccttc cgctaaaaag gcaatcgtct aaagctggtc 360
ccttttgggag tattcacggg gctgtccaat ctactaagc ttgacattag tgagaataag 420
attgtcattt tactagacta catgttccaa gatctacata acctgaagtc tctagaagtg 480
ggggacaatg atttggttta tatatcacac agggcattca gtgggcttct tagcttggag 540
cagctcacc caggagaaatg caacttaaca gcagtaccaa cagaagccct ctcccacctc 600
cgcagcctca tcagcctgca tctgaagcat ctcaatatca acaatatgcc tgtgtatgcc 660
tttaaaagat tgttccacct gaaacaccta gagattgact attggccttt actggatatg 720
atgcctgcca atagcctcta cggcttcaac ctacatccc ttccagtcac caacaccaat 780
ctgtctactg tacccttctt tgcctttaa cactgggtat acctgactca ccttaacctc 840
tctacaatc ccatcagcac tattgaagca ggcatgttct ctgacctgat ccgccttcag 900
gagcttcata tagtgggggc ccagcttcgc accattgagc ctactcctt ccaagggtc 960
cgcttcttac gcgtgtctca tgtgtctcag aacctgctgg aaactttgga agagaatgtc 1020
tttctctccc ctagggtctt ggaggtcttg agcattaaca acaacctctt ggctgtgac 1080
tgccgccttc tctggatctt gcagcgacag cccaccctgc agtttgggtg ccagcaacct 1140
atgtgtgctg gccagacac catccgtgag aggtctttca aggatttcca tagcactgcc 1200
ctttcttttt actttacctg caaaaaaccc aaaatccgtg aaaagaagtt gcagcatctg 1260
ctagtagatg aagggcagac agtccagcta gaatgcagtg cagatggaga cccgcagcct 1320
gtgatttctt ggtgacacc ccgaagcgtt tcatcaccac caagtccaat ggaagagcca 1380
ccgtgttggg tgatggcacc ttggaaatcc gctttgccca ggatcaagac agcgggatgt 1440
atgtttgcat cgctagcaat gctgtctggga atgatacctt cacagcctcc ttaa 1494

```

<210> 8
<211> 497
<212> PRT
<213> homo sapiens

<400> 8

Met	Leu	His	Thr	Ala	Ile	Ser	Cys	Trp	Gln	Pro	Phe	Leu	Gly	Leu	Ala
1				5					10					15	
Val	Val	Leu	Ile	Phe	Met	Gly	Ser	Thr	Ile	Gly	Cys	Pro	Ala	Arg	Cys
			20					25					30		
Glu	Cys	Ser	Ala	Gln	Asn	Lys	Ser	Val	Ser	Cys	His	Arg	Arg	Arg	Leu
		35				40					45				
Ile	Ala	Ile	Pro	Glu	Gly	Ile	Pro	Ile	Glu	Thr	Lys	Ile	Leu	Asp	Leu
	50					55					60				
Ser	Lys	Asn	Arg	Leu	Lys	Ser	Val	Asn	Pro	Glu	Glu	Phe	Ile	Ser	Tyr
65				70					75					80	
Pro	Leu	Leu	Glu	Glu	Ile	Asp	Leu	Ser	Asp	Asn	Ile	Ile	Ala	Asn	Val
			85					90						95	
Glu	Pro	Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Ser	Leu	Arg	Leu
			100					105					110		
Lys	Gly	Asn	Arg	Leu	Lys	Leu	Val	Pro	Leu	Gly	Val	Phe	Thr	Gly	Leu
		115					120				125				
Ser	Asn	Leu	Thr	Lys	Leu	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val	Ile	Leu
	130					135					140				
Leu	Asp	Tyr	Met	Phe	Gln	Asp	Leu	His	Asn	Leu	Lys	Ser	Leu	Glu	Val
145				150					155					160	
Gly	Asp	Asn	Asp	Leu	Val	Tyr	Ile	Ser	His	Arg	Ala	Phe	Ser	Gly	Leu
			165					170						175	
Leu	Ser	Leu	Glu	Gln	Leu	Thr	Leu	Glu	Lys	Cys	Asn	Leu	Thr	Ala	Val
			180					185					190		
Pro	Thr	Glu	Ala	Leu	Ser	His	Leu	Arg	Ser	Leu	Ile	Ser	Leu	His	Leu
		195					200					205			
Lys	His	Leu	Asn	Ile	Asn	Asn	Met	Pro	Val	Tyr	Ala	Phe	Lys	Arg	Leu
	210					215					220				
Phe	His	Leu	Lys	His	Leu	Glu	Ile	Asp	Tyr	Trp	Pro	Leu	Leu	Asp	Met


```

ccccggcctgg cccggccgcta cttctctgggca gtgccccgagg gcgagttctc ctgtgagccg 840
cccctcattg cccgccacac gcagcgccctc tgggtgctgg aaggccagcg ggccacgctg 900
cgggtgccggg ccctgggtga ccccgcgccct accatgcact gggtcgggtcc tgacgaccgg 960
ttgggttgga actcctcccg agcccgggct ttcccacacg ggaccttaga gattgggggtg 1020
accggcgctg gggacgctgg gggctacacc tgcacgcga ccaaccctgc tgggtgaggcc 1080
acagcccag tagaactgcg ggtgctggcc ttgccccatg gtgggaacag cagtgccgag 1140
ggggggccgcc ccggggccctc ggacatcgcc gcctccgctc gcactgctgc cgagggtgag 1200
gggacgctgg agtctgagcc agccgtgcag gtgacggagg tgaccgccac ctcagggtg 1260
gtgagctggg gtcccgggcg gccagccgac ccagtgtgga tgttccaaat ccagtacaac 1320
agcagcgaag atgagaccct catctaccgg attgtcccag cctccagcca ccacttcctg 1380
ctgaagcacc tcgtccccgg cgtgactat gacctctgcc tgctggcctt gtcaccggcc 1440
gctggggcct ctgacctcac ggccaccagg ctgctgggct gtgcccattt ctccacgctg 1500
ccggcctcgc ccctgtgcca cggcctgcag gccacgtgc tgggcgggac cctgaccgtg 1560
gccgtggggg gtgtgctggt ggtgcctta ctggtcttca ctgtggcctt gctgggtcgg 1620
ggccgggggg ccggaatgg ccgcctcccc ctcaagctca gccacgtcca gtcccagacc 1680
aatggaggcc ccagcccac acccaaggcc caccgcgcg ggagccccc gccccggccg 1740
cagcgcagct gctctctgga cctgggagat gccgggtgct acggttatgc caggcgccctg 1800
ggaggagctt gggcccgacg gagccactct gtgcatgggg ggctgctcgg ggcagggtgc 1860
cggggggtag gaggcagcgc cgagcggctg gaagagagtg tgggtgtga 1908

```

```

<210> 10
<211> 635
<212> PRT
<213> homo sapiens

```

```

<400> 10
Met Ala Pro Pro Leu Leu Leu Leu Leu Leu Ala Ser Gly Ala Ala Ala
  1          5          10          15
Cys Pro Leu Pro Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Ser Thr
  20          25          30
Leu Cys Ala His Arg Gly Leu Leu Phe Val Pro Pro Asn Val Asp Arg
  35          40          45
Arg Thr Val Glu Leu Arg Leu Ala Asp Asn Phe Ile Gln Ala Leu Gly
  50          55          60
Pro Pro Asp Phe Arg Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser
  65          70          75          80
Arg Asn Ala Ile Thr Arg Ile Gly Ala Arg Ala Phe Gly Asp Leu Glu
  85          90          95
Ser Leu Arg Ser Leu His Leu Asp Gly Asn Arg Leu Val Glu Leu Gly
  100         105         110
Thr Gly Ser Leu Arg Gly Pro Val Asn Leu Gln His Leu Ile Leu Ser
  115         120         125
Gly Asn Gln Leu Gly Arg Ile Ala Pro Gly Ala Phe Asp Asp Phe Leu
  130         135         140
Glu Ser Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu Arg Gln Val
  145         150         155         160
Pro Trp Ala Gly Ile Gly Ala Met Pro Ala Leu His Thr Leu Asn Leu
  165         170         175
Asp His Asn Leu Ile Asp Ala Leu Pro Pro Gly Ala Phe Ala Gln Leu
  180         185         190
Gly Gln Leu Ser Arg Leu Asp Leu Thr Ser Asn Arg Leu Ala Thr Leu
  195         200         205
Ala Pro Asp Pro Leu Phe Ser Arg Gly Arg Asp Ala Glu Ala Ser Pro
  210         215         220
Ala Pro Leu Val Leu Ser Phe Ser Gly Asn Pro Leu His Cys Asn Cys
  225         230         235         240

```


Glu Leu Leu Trp Leu Arg Arg Leu Ala Arg Pro Asp Asp Leu Glu Thr
 245 250 255
 Cys Ala Ser Pro Pro Gly Leu Ala Gly Arg Tyr Phe Trp Ala Val Pro
 260 265 270
 Glu Gly Glu Phe Ser Cys Glu Pro Pro Leu Ile Ala Arg His Thr Gln
 275 280 285
 Arg Leu Trp Val Leu Glu Gly Gln Arg Ala Thr Leu Arg Cys Arg Ala
 290 295 300
 Leu Gly Asp Pro Ala Pro Thr Met His Trp Val Gly Pro Asp Asp Arg
 305 310 315 320
 Leu Val Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu
 325 330 335
 Glu Ile Gly Val Thr Gly Ala Gly Asp Ala Gly Gly Tyr Thr Cys Ile
 340 345 350
 Ala Thr Asn Pro Ala Gly Glu Ala Thr Ala Arg Val Glu Leu Arg Val
 355 360 365
 Leu Ala Leu Pro His Gly Gly Asn Ser Ser Ala Glu Gly Gly Arg Pro
 370 375 380
 Gly Pro Ser Asp Ile Ala Ala Ser Ala Arg Thr Ala Ala Glu Gly Glu
 385 390 395 400
 Gly Thr Leu Glu Ser Glu Pro Ala Val Gln Val Thr Glu Val Thr Ala
 405 410 415
 Thr Ser Gly Leu Val Ser Trp Gly Pro Gly Arg Pro Ala Asp Pro Val
 420 425 430
 Trp Met Phe Gln Ile Gln Tyr Asn Ser Ser Glu Asp Glu Thr Leu Ile
 435 440 445
 Tyr Arg Ile Val Pro Ala Ser Ser His His Phe Leu Leu Lys His Leu
 450 455 460
 Val Pro Gly Ala Asp Tyr Asp Leu Cys Leu Leu Ala Leu Ser Pro Ala
 465 470 475 480
 Ala Gly Pro Ser Asp Leu Thr Ala Thr Arg Leu Leu Gly Cys Ala His
 485 490 495
 Phe Ser Thr Leu Pro Ala Ser Pro Leu Cys His Ala Leu Gln Ala His
 500 505 510
 Val Leu Gly Gly Thr Leu Thr Val Ala Val Gly Gly Val Leu Val Ala
 515 520 525
 Ala Leu Leu Val Phe Thr Val Ala Leu Leu Val Arg Gly Arg Gly Ala
 530 535 540
 Gly Asn Gly Arg Leu Pro Leu Lys Leu Ser His Val Gln Ser Gln Thr
 545 550 555 560
 Asn Gly Gly Pro Ser Pro Thr Pro Lys Ala His Pro Pro Arg Ser Pro
 565 570 575
 Pro Pro Arg Pro Gln Arg Ser Cys Ser Leu Asp Leu Gly Asp Ala Gly
 580 585 590
 Cys Tyr Gly Tyr Ala Arg Arg Leu Gly Gly Ala Trp Ala Arg Arg Ser
 595 600 605
 His Ser Val His Gly Gly Leu Leu Gly Ala Gly Cys Arg Gly Val Gly
 610 615 620
 Gly Ser Ala Glu Arg Leu Glu Glu Ser Val Val
 625 630 635

<210> 11
 <211> 2518
 <212> DNA
 <213> homo sapiens

<400> 11

cgattccttg	ggacgcctgg	gaaaggaagt	tccgggaccc	tccctgctct	cggtcctcct	60
ccgcttcctg	cctcatgcct	caccttgctc	ccagcgcctg	gactccccct	taactgcttg	120
ggaaatgtga	cctttgctct	ggggggcctg	gccctgcagg	ccccaacctt	ccctcatctc	180
tggcggccct	cttgggcctc	tgaccagcc	cctccccggg	ccaggctcac	agaagctggc	240
ttctgggact	gtcctgggce	caagtgggca	cctgcgccag	ccccacctgt	gcctgggctg	300
tggccccctt	ctacagggcg	ctcaccatgg	ccccgccgct	cctgctgctg	ctgctggcca	360
gtggagcggc	cgcctgcccg	ctgccctgcg	tctgccagaa	cctgtccgag	tcgctcagca	420
ccctctgtgc	ccaccgaggg	ctgctgtttg	tgccgcccaa	cgtggaccgg	cgcacagtgg	480
agctgcggt	ggctgacaac	ttcatccagg	ccctggggcc	ccctgacttc	cgcaacatga	540
cgggactggg	ggacctgaca	ctgtctcgca	atgccatcac	ccgcattggg	ggcgcgcct	600
ttggggacct	cgagagcctg	cgttcctcc	accttgacgg	caacaggctg	gtggagctgg	660
gcaccgggag	cctccggggc	cccgctcaatc	tgcagcacct	catcctcagc	ggcaaccagc	720
tgggcccgc	cgcgcgggga	gccttcgacg	acttcctaga	gagcctggag	gacctggacc	780
tgtcctacaa	caacctccgg	caggtgccct	gggcccgc	cggcgccatg	cctgccctgc	840
acaccctcaa	cctggaccat	aaccttattg	acgcactgcc	cccaggcgcc	ttcgcccagc	900
tcggtcagct	ctcccgccctg	gacctcacct	ccaaccgcct	ggccacgctg	gctccggacc	960
cgtttttctc	tcgtgggctg	gatgcagagg	cctctcccgc	ccccctggtg	ctgagcttta	1020
gcggaaccc	cctgcaactg	aactgtgagc	tgtgtgggt	gcgggcggtg	gcgcgcccg	1080
acgacctgga	aacgtgcgcc	ccccgcgccg	gcttgccggg	ccgctacttc	tgggcagctg	1140
ccgagggcga	gttctcctgt	gagccgcccc	tcattgcccg	ccacacgcag	cgctcttggt	1200
tgttggaagg	ccagcggggc	acgctgcggt	gccgggccct	gggtgacccc	gcgcctacca	1260
tgactgggt	cgtcctgac	gaccggttgg	ttggcaactc	ctcccgagcc	cgggctttcc	1320
ccaacgggac	cttagagatt	ggggtgaccg	gcgtggggga	cgtggggggc	tacacctgca	1380
tcgccaccaa	ccctgctggt	gagccacag	cccagtaga	actgcgggtg	ctggccttgc	1440
cccatgggtg	gaacagcagt	gccgaggggg	gccgcccggg	gccctcgga	atcgccgcct	1500
ccgctcgcac	tgtgcccag	gggtgagggga	cgtggagtc	tgagccagcc	gtgcaggtga	1560
cggaggtgac	cgccacctca	gggctggtga	gctgggggtc	cgggcggcca	gccgaccag	1620
tgtggatgtt	ccaaatccag	tacaacagca	gcgaagatga	gacctcatc	taccggattg	1680
tcccagcctc	cagccaccac	ttcctgctga	agcacctcgt	ccccggcgct	gactatgacc	1740
tctgcctgct	ggccttgcta	cgggcgcgtg	ggcctctga	cctcacggcc	accaggctgc	1800
tgggctgtgc	ccattttctc	acgctgcggg	cctcgcccct	gtgccacgcc	ctgcaggccc	1860
acgtgctggg	cgggacctg	accgtggccg	tgggggggtg	gctgggtggc	gccttactgg	1920
tcttcaactg	ggccttgctg	gttcggggcc	ggggggccgg	aaatggcgcc	ctccccctca	1980
agctcagcca	cgtccagtc	cagaccaatg	gaggccccag	ccccacaccc	aaggcccacc	2040
cgcgcgggag	ccccccgccc	cggccgcagc	gcagctgctc	tctggacctg	ggagatgccg	2100
ggtgctacgg	ttatgccagg	cgcctgggag	gagcttgggc	ccgacggagc	cactctgtgc	2160
atggggggct	gctcggggca	gggtgcccgg	gggtaggagg	cagcgccgag	cggctggaag	2220
agagtgtggt	gtgatggacg	ggcagcttcc	tgtgtgctcc	aagggatgag	cctcgtgggg	2280
cagagggccc	ggggccgccc	cctggcctgg	gagtcctcc	ctggttttta	ttctcagtac	2340
ctcaggctcc	cctgtgtact	tggaggggca	gggagccctt	tcctcggttc	tggcctccag	2400
accagggtaa	gggcaggccc	ctccaacagg	tgtcacagc	caccgaggca	ggggctgcag	2460
ccaccactg	ggagtcttgt	ttttatttat	aataaaattg	ttggggacac	mwmaaaaa	2518